31. (Once Amended) A computer readable memory according to claim 39 wherein said ranking module includes a van der Waals scoring function component.

32. (Once Amended) A computer readable memory according to claim 39 wherein said ranking module includes an atomic solvation scoring function component.

33. (Once Amended) A computer readable memory according to claim 39 wherein said ranking module includes a hydrogen bond scoring function component.

34. (Once Amended) A computer readable memory according to claim 39 wherein said ranking module includes a secondary structure scoring function component.

35. (Once Amended) A computer readable memory according to claim 39 that further assess the correspondence between potential energy test results and theoretical potential energy data.

Please add the following new claims.

36. (New) A computer readable memory that upon execution by a computer processor carries out the following functions:

      a) alters at least one supersecondary structure parameter value of a protein backbone structure;

      b) correlates a group of potential amino acids for residue positions of said protein backbone structure; and

      c) analyzes the interaction of each of said amino acids with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences.

37. (New) A computer readable memory that upon execution by a computer processor carries out the following functions:

      a) alters at least one structure parameter value of a protein backbone structure;

      b) correlates a group of potential rotamers for residue positions of said protein backbone structure; and

      c) analyzes the interaction of each of said rotamers with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences.

38. (New) A computer readable memory that upon execution by a computer processor carries out the following functions:

 a) alters at least one structure parameter value of a protein backbone structure;

 b) correlates a group of potential amino acids for residue positions of said protein backbone structure; and

 c) analyzes the interaction of each of said amino acids with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences.

39. (New) A computer readable memory according to claims 30, 36, 37, or 38 wherein said analyzing step comprises a ranking module.

40. (New) A computer readable memory that upon execution by a computer processor carries out the following functions:

 (A) receiving a protein backbone structure with variable residue positions;

 (B) altering at least one supersecondary structure parameter value of said protein backbone structure prior to establishing a group of potential amino acids;

 (C) establishing a group of potential amino acids for each of said variable residue positions, wherein a first group for a first variable position has a first set of at least two amino acid side chains, and wherein a second group for a second variable position has a second set of at least two different amino acid side chains; and

 (D) analyzing the interaction of all or part of each of said amino acids with all or part of the remainder of said protein backbone structure to generate a set of optimized protein sequences.

41. (New) A computer readable memory according to claim 40 wherein said first and second sets of amino acids are different.

42. (New) A computer readable memory according to claim 40 wherein said first and second sets of amino acids are the same.

643. (New) A computer readable memory that upon execution by a computer processor carries out the following functions:

   a) receiving a protein backbone structure with variable residue positions;

   b) altering at least one supersecondary structure parameter value of said protein backbone structure prior to establishing a group of potential rotamers positions;

   c) establishing a group of potential rotamers for each of said variable residue positions, wherein the group for at least one variable residue position has rotamers of at least two different amino acid side chains, and wherein at least one of said amino acid side chains is from a hydrophilic amino acid; and,

   d) analyzing the interaction of each of said rotamers with all or part of the remainder of said protein to generate a set of optimized protein sequences, wherein said analyzing step includes the use of at least one scoring function.

44. (New) A computer readable memory according to claim 43 wherein said first and second sets of rotamers are different.

45. (New) A computer readable memory according to claim 43 wherein said first and second sets of rotamers are the same.

946. (New) A computer readable memory according to claim 43 wherein said hydrophilic amino acid is selected from the group consisting of serine, threonine, aspartic acid, asparagine, glutamine, glutamic acid, arginine, lysine, and histidine.

1047. (New) A computer readable memory according to claims 40 or 43 wherein said analyzing step comprises a ranking module.

48. (New) A computer readable memory according to claims 40-47 further comprising physically generating at least one member of said set of optimized protein sequences and experimentally testing said sequence for a desired function.

REMARKS

Claims 30-35 are pending in this application. Claims 2-29 have been cancelled. Claims 36-39 have been added. Support for the addition of the new Claims 36-39 may be